

CLAIMS

1. A Glutathione-S-transferase (GST) comprising the amino acid sequence depicted as SEQ ID No. 10 or a variant GST having at least 80% identity therewith with the  
5 *proviso* that said variant GST does not comprise the amino acid sequence depicted as SEQ ID No. 36.
2. A GST or variant GST according to claim 1 which is capable of conferring resistance and/or tolerance to a herbicide which comprises fomesafen and/or acifluorfen.  
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3. A polynucleotide comprising a region which encodes a GST or a variant GST according to claim 1 or claim 2.
4. A polynucleotide according to claim 3 comprising the sequence depicted as SEQ ID  
15 No. 14.
5. A polynucleotide sequence which is the complement of one which binds to a polynucleotide according to claim 3 or claim 4 at a temperature of between 60°C and 65°C in 0.3 strength citrate buffered saline containing 0.1% SDS followed by rinsing  
20 at the same temperature with 0.3 strength citrate buffered saline containing 0.1% SDS wherein said polynucleotide sequence still encodes a functional GST with the *proviso* that said polynucleotide sequence is not the sequence depicted as SEQ ID No. 38.
6. A protein comprising the amino acid sequence depicted as SEQ ID No. 1 or a protein  
25 variant having at least about 70% identity therewith wherein said protein or variant is capable of catalysing the addition of Beta-alanine onto gamma glutamylcysteine.
7. A protein variant according to claim 6 having a Km for Beta-alanine which is less  
30 than the said variants Km for glycine when calculated using the same method.

8. A protein variant according to claim 7 having a  $K_m$  for Beta-alanine which is less than or equal to about 0.8mM and a  $K_m$  for glycine which is higher than 0.8mM when calculated using the same method.
- 5 9. A protein variant according to claim 7 or 8 which variant comprises an amino acid sequence selected from the group depicted as SEQ ID No. 2, 3, 4 or 5.
10. A polynucleotide comprising a region encoding the protein or protein variant according to any one of claims 6 to 9.
- 10 11. A polynucleotide according to claim 10 which comprises the sequence depicted as SEQ ID No. 6.
12. A polynucleotide comprising a first region comprising a polynucleotide according to any one of claims 3 to 5 and a second region comprising a polynucleotide according to claim 10 or 11.
- 15 13. A polynucleotide according to claim 12 wherein said first region comprises a polynucleotide encoding the amino acid sequence depicted as SEQ ID No. 10 and said second region comprises a polynucleotide encoding the amino acid depicted as SEQ ID No. 1.
- 20 14. A DNA construct comprising in sequence a plant operable promoter operably linked to a polynucleotide according to any one of claims 3, 4, 5, 10, 11, 12 or 13 operably linked to a transcription termination region.
- 25 15. A method of providing plants which are resistant and/or tolerant to an agrochemical comprising:
- (a) inserting into the genome of plant material a polynucleotide or a polynucleotide sequence according to any one of claims 3, 4, 5, 10, 11, 12 or 13 or a DNA construct according to claim 14; and
- 30 (b) regenerating plants or plant parts therefrom; and

(c) applying to said plants or plant parts an amount of said agrochemical which is phytotoxic to control like plants and selecting those plants or plant parts which are resistant to said agrochemical.

- 5 16. A method according to claim 15 wherein the polynucleotide inserted into said material encodes an amino acid sequence depicted as SEQ ID No. 10.
17. A method of providing plants which are resistant and/or tolerant to an agrochemical comprising:
- 10 (a) inserting into the genome of plant material from a plant which provides for the production of a functional GST, a polynucleotide according to any one of claims 10 to 13 or a DNA construct according to claim 14; and
- (b) regenerating plants or plant parts therefrom; and
- 15 (c) applying to said plants or plant parts an amount of said agrochemical which is phytotoxic to control like plants and selecting those plants or plant parts which are resistant to said agrochemical.
18. A method according to any one of claims 15 to 17 wherein said agrochemical comprises fomesafen and/or acifluorfen.
- 20 19. Plants or plant parts obtained according to the method of any one of claims 15 to 18.
20. Plants or plant parts according to claim 19 which are soybean plants or plant parts.
- 25 21. Use of a polynucleotide according to any one of claims 3, 4, 5, 10, 11, 12 or 13 or a DNA construct according to claim 14 in a method of producing plants which are resistant and/or tolerant to a herbicide comprising fomesafen and/or acifluorfen.
22. A method of providing a plant with a further desired agronomic trait comprising:
- 30 (a) inserting into the genome of plant material from a plant or plant part according to claim 19 or 20 a polynucleotide which provides for the desired agronomic trait; and regenerating plants or plant parts from said material; or

- (a) crossing a first plant or plant part according to claim 19 or claim 20 with a second plant which provides for said desired agronomic trait; and
- (b) selecting those resultant plants which contain said further desired agronomic trait.

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23. A method according to claim 22 wherein said further desired agronomic trait provides resistance to a herbicide which comprises glyphosate or a salt thereof.

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24. A method of selectively controlling weeds in a field said field comprising crop plants and weeds said method comprising applying to said field an agriculturally acceptable formulation of an agrochemical comprising fomesafen and/or acifluorfen wherein the said crop plants are the plants according to claim 19 or 20.

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25. Use of an agrochemical comprising fomesafen and/or acifluorfen to selectively control weeds in a field which field comprises crop plants and weeds comprising applying to said field an agriculturally acceptable formulation of said agrochemical in an amount which is sufficient to be phytotoxic to said weeds but not said crop plants characterised in that said crop plants are the plants according to claim 19 or 20.

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26. A protein comprising the sequence depicted as SEQ ID No. 10 or a protein variant having a Smith Waterman score greater than 766 calculated using the FASTA3 algorithm wherein the said protein variant still encodes a Glutathione-S-transferase.

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27. A protein comprising the sequence depicted as SEQ ID No. 1 or a protein variant having a Smith-Waterman score greater than 2152 calculated using the FASTA3 algorithm wherein the said protein variant still encodes a homoglutathione synthetase.